GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 1, 2005, 14:20:08 ; Search time 40 Seconds
(without alignments)
582.111 Million cell updates/sec

Title: US-10-629-329A-2
Perfect score: 1322
Sequence: 1 MSGGCDAGEGDCCSRRCGAQD.........SMKKVGLDFSQLPVGENGIV 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	495	37.4	244	2	S57042	hypothetical prote
2	431.5	32.6	284	2	T27523	hypothetical prote
3	274.5	20.8	192	2	T39191	conserved hypothet
4	215.5	16.3	209	2	A69864	conserved hypothet
5	192.5	14.6	208	1	H70469	L-fuculose-phospha
6	166	12.6	205	2	D83436	probable sugar ald
7	156.5	11.8	191	1	C69054	L-fuculose-phospha
8	152	11.5	181	1	A64477	L-fuculose-phospha
9	151	11.4	254	1	A72396	L-ribulose-phospha
10	145	11.0	231	2	S47804	L-ribulose-phospha
11	144	10.9	218	2	E82587	conserved hypothet
12	142	10.7	227	2	A95238	probable sugar iso
13	141	10.7	231	2	AI0977	l-fuculose-phospha
14	140.5	10.6	244	2	AC3513	L-ribulose-phospha
15	137	10.4	234	2	B98102	L-ribulose-phospha
16	132	10.0	243	2	G90586	sugar isomerase Sg
17	131	9.9	228	2	AD1052	probable class II
18	131	9.9	231	2	G83883	L-ribulose-5-phosp
19	130	9.8	229	2	E69587	L-ribulose-phospha
20	129.5	9.8	243	2	H64108	L-ribulose-phospha
21	129	9.8	228	2	S56423	L-ribulose-phospha
22	128.5	9.7	231	2	AI0271	L-ribulose-phospha
23	128	9.7	228	2	F91275	probable epimerase
24	128	9.7	228	2	F86116	probable epimerase
25	127	9.6	230	2	B82484	sugar isomerase Sg
26	126	9.5	242	2	S73671	L-ribulose-phospha
27	123	9.3	211	1	H84275	fuculose-1-phospha
28	122	9.2	189	1	E71241	L-fuculose-phospha
29	120.5	9.1	215	1	ADECFP	L-fuculose-phospha
30	120.5	9.1	231	2	AB0404	L-ribulose-phospha
31	119.5	9.0	215	2	F85931	L-fuculose-1-phosp
32	119.5	9.0	215	2	D91086	L-fuculose-1-phosp
33	119	9.0	216	1	C64081	L-fuculose-phospha
34	117	8.9	225	2	B96013	probable aldolase,
35	116.5	8.8	215	2	AH0862	fuculose-1-phospha
36	116.5	8.8	248	1	ISEB4T	L-ribulose-phospha
37	114.5	8.7	212	2	C95253	L-fuculose phospha
38	114.5	8.7	217	2	A98118	L-fuculose-phospha
39	112.5	8.5	233	2	B97065	ribulose-5-phospha
40	111.5	8.4	224	2	AF3646	l-fuculose phospha
41	111.5	8.4	231	1	ISECP4	L-ribulose-phospha
42	111.5	8.4	231	2	A85488	L-ribulose-5-phosp
43	111.5	8.4	231	2	A90637	L-ribulose-5-phosp
44	109.5	8.3	215	1	E72546	L-fuculose-phospha
45	109.5	8.3	231	2	AB0515	L-ribulose-5-phosp

ALIGNMENTS

RESULT 1
S57042
hypothetical protein YJR024c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein J1545; hypothetical protein YJR83.18
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S57042; S57039; S55213; S60503; S61120
R;Zagulski, M.; Babinska, B.; Gromadka, R.; Migdalski, A.; Rytka, J.; Sulicka, J.; Herbe
submitted to the Protein Sequence Database, September 1995
A;Reference number: S57040
A;Accession: S57042
A;Molecule type: DNA
A;Residues: 1-244 <HUA>
A;Cross-references: UNIPROT:P47095; EMBL:Z49524; MIPS:YJR024c
R;de Haan, M.; Grivell, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56771
A;Accession: S57039
A;Molecule type: DNA
A;Residues: 44-244 <ZAG>
A;Cross-references: EMBL:Z49524; MIPS:YJR024c
R;de Haan, M.; Smits, P.H.M.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A;Reference number: S55183
A;Accession: S55213
A;Molecule type: DNA
A;Residues: 44-244 <DEH>
A;Cross-references: EMBL:X87611; NID:g854567; PIDN:CAA60947.1; PID:g854598
R;Zagulski, M.; Babinska, B.; Gromadka, R.; Migdalski, A.; Rytka, J.; Sulicka, J.; Herbe
Yeast 11, 1179-1186, 1995
A;Title: The sequence of 24.3 kb from chromosome X reveals five complete open reading fr
A;Reference number: S60503; MUID:96109930; PMID:8619316
A;Accession: S60503
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-244 <ZAF>
A;Cross-references: EMBL:X87297; NID:g1129159; PIDN:CAA60719.1; PID:e183285; PID:g112916
C;Genetics:
A;Cross-references: SGD:S0003785
A;Map position: 10R

Query Match 37.4%;   Score 495;   DB 2;   Length 244;
Best Local Similarity 45.9%;   Pred. No. 4e-37;
Matches 107;   Conservative 37;   Mismatches 69;   Indels 20;   Gaps 7;

```
Qy  18  AQDKEHPRYLIPELCKQFYHLGWTGTGGISLK--HGDEIYIAPSGVQKERIQPEDMFV  75
           :  ||||:|| |||||||||||||  :::||:||||::: |:|| ::
Db  10  SDDPCHPANLICTLCKQFFHNWCTGTGGGISIKDPNTNYYLAPSGVQKEKMIPEDLFV  69

Qy  76  CDINEKD-ISGPSPSKKLKKSQCTPLFMNAYTMRGAGAVIHTHSKAAVMATLLPPGREFK 134
          |:| :  :|||:|: :|||::::|| || :::|||||:||||:: ||::::||:|
Db  70  MDAQTLEYLRSP---KLYKPSACTPLFLACYQKKNAGAIIHTHSQNAVICSLLF-GDEFR 125
```

Matches   75; Conservative   29; Mismatches   76; Indels   21; Gaps   6;

Qy   27 LIPELCKQFYHLGWVT-GTGGGISLKHGDEIYIAPSGVQKERIQPEDMFVCDINEKDISG 85
          ||||| ||||| |||| : || ||| ||: : :   ::   : ::||:
Db   9 LILELIPHFYSLGWMKFGSGYAICV------------KDRVQRDFTTENDIVTFNLSN 54

Qy   86 PSPSKKLKKSQCTPLFMNAYTMRGAGAVIHTHSKAAVMATLLFPGREFKITHQEMIKGIK 145
          : :||| : ||| || : : || | :|| ||:|| |||| ::||:
Db   55 QSVTKDL--VNWAYIFSWVLSNMDAVACIYSTSVAAVGASMY--NEKFTTQSKEMIKGIP 110

Qy   146 KCT-SGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWGETW 204
          | ||||| ||| | |: : : || | ||:   :|:| |:|||||| || |
Db   111 KGNPSAGYLCCFDTLEVPIIHN-GDSKTILDELKKVIELYPQTCAVLIRGHGVIGWGATW 169

Qy   205 EKAKTMCECYDLFDIAVSMK 225
          | |||||:||||||:|| |:
Db   170 EKSKTQMECYEYLFELDYKLK 190

RESULT 4
A69864
conserved hypothetical protein ykrY - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: A69864
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fujita, M.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y.,M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: A69864
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-209 <KUN>
A;Cross-references: UNIPROT:O31668; GB:Z99111; GB:AL009126; NID:g2633699; PIDN:CAB13234
A;Experimental source: strain 168
C;Genetics:
A;Gene: ykrY
C;Superfamily: L-ribulose-phosphate 4-epimerase

Query Match   16.3%; Score 215.5; DB 2; Length 209;
Best Local Similarity   32.4%; Pred. No. 5.6e-12;
Matches   66; Conservative   32; Mismatches   87; Indels   19; Gaps   7;

Qy   28 IPELCKQFYHLGWVTGTGGGISLKHGDE---IYIAPSGVQKERIQPEDMFVCDIN-EKDI 83
          | : | : || |: | || || :: : : | |: | :   :
Db   11 LAEVKRELAERDWFPATSGNLSIKVTDEPLTFLVTASGKDKRKETVEDFLLVDQNGEPAE 70

Qy   84 SGPSPSKKLKKSQCTPLFMNAYTMRGAGAVIHTHSKAAVMATLLFPGREFKITH--QEMI 141
          ||| : | | :| :| || | | | || |::| || | |:|
Db   71 SGHS---LKPSAETLLHTHLYNKTNAGCCLHVTVNNNVISELY-GDQKKITFKGQEII 125

Qy   142 KGIKKCTSGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWG 201
          ||: | : |:|:||: |: ||:|| : | : :   :| |:||| |
Db   126 KAL------GlWEENAEVTVPIIENPAHIPTLAALFAEEISE--DSGAVLIRNHGITAWG 177

Qy   202 ETWEKAKTMCECYDLFDIAVSMK 225
          :||| | || |||||||||:|:|
Db   178 KTAFEAKRVLEAYEFLFSYHLKLK 201

RESULT 5

Qy   135 ITHQEMIKGI--------KKCTSGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYP 185
          :|| ||||| :: :   : |||| |:
Db   126 IANIEQIKAIPSGKVDPVTKKPMALSFF---DTLKIPIIENMAHEDELIDDLlHKTFKDYP 182

Qy   186 DSCAVLVRRHGVYVWGETWEKAKTMCECYDLFDIAVSMKKVGLDPSQLPVGE 238
          |:|| |:|||| |:|| |:|||||||||||:||||||| |:
Db   183 DTCAVIFSWRGIFWGPTIDKAKIFNEAIDYLMELAIKMYQMGI-PPDCGIGE 234

RESULT 2
T27523
hypothetical protein ZC373.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A;Accession: T27523
R;Kershaw, J.
submitted to the EMBL Data Library, April 1995
A;Reference number: Z20382
A;Accession: T27523
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-284 <WIL>
A;Cross-references: UNIPROT:Q23261; EMBL:Z49131; PIDN:CAA88977.1; GSPDB:GN00028; CESP:ZC
C;Genetics:
A;Gene: CESP:ZC373.5
A;Map position: X
A;Introns: 26/3; 75/2; 114/1; 236/2

Query Match   32.6%; Score 431.5; DB 2; Length 284;
Best Local Similarity   39.9%; Pred. No. 2.6e-31;
Matches   87; Conservative   34; Mismatches   76; Indels   21; Gaps   1;

Qy   30 ELCKQFYHLGWVTGTGGGISLKHGDEIYIAPSGVQKERIQPEDMFVCDINEKDISGPSPS 89
          || |||||||| |:||| :|| ||||||||| |||:|| ||:|| :| | | |
Db   35 ELMIQFYKLGWMRGSGGAMGCISGGSELMISSALQKERIREQDVFVYNMKDKTEVQRPPN 94

Qy   90 KKLKKSQCTPLFMNAYTMRGAGAVIHTHSKAAVMATLLFPGREFKITHQEMIKGIKKCTS 149
          ||| : | | |: ||||: | : :| | |||||| : | | |
Db   95 KRITVSSCSVLFSLIMKETGBECVIHTHSKCANLITQLIKSNVFEISHQEVIKGIYDPFS 154

Qy   150 GGYYRYDDMLVVPIIENTPEEKGL----------------KDRMAHAMNEYPDSC 188
          ||||| ||| :||||| ::| | | ::|:
Db   155 GKALKYSDTLTIPIIDNMPSESQLLVCAINRSPMQPDCFINIALFQEPIRGVLENYPQAI 214

Qy   189 AVLVRRHGVYVWGETWEKAKTMCECYDLFDIAVSMK 226
          |||||:||| |:|| |::||||||||||||||||:
Db   215 AVLVRNHGLFVWGPTWESTKIMTECIDYLLELSIEMLK 252

RESULT 3
T39191
conserved hypothetical protein SPAC9.06c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
A;Accession: T39191
R;Wedler, H.; Duesterhoeft, A.; Lyne, M.H.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z21834
A;Accession: T39191
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-192 <WED>
A;Cross-references: UNIPROT:Q9UT22; EMBL:AL121764; PIDN:CAB57424.1; GSPDB:GN00066; SPDB:
C;Genetics:
A;Gene: SPDB:SPAC9.06c
A;Map position: 1
A;Introns: 27/2; 53/2; 73/2; 129/1

Query Match   20.8%; Score 274.5; DB 2; Length 192;
Best Local Similarity   37.3%; Pred. No. 2.4e-17;

H70469
L-fuculose-phosphate aldolase homolog - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: H70469
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
v.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: H70469
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-208 <AQF>
A;Cross-references: UNIPROT:O67788; GB:AE000766; NID:g2984216; PIDN:AAC077
A;Experimental source: strain VF5
C;Genetics:
A;Gene: fucA2
C;Superfamily: L-ribulose-phosphate 4-epimerase

Query Match   14.6%;   Score 192.5;   DB 1;   Length 208;
Best Local Similarity   25.1%;   Pred. No. 6.6e-10;
Matches   53; Conservative 37; Mismatches 94; Indels 27; Gaps   5;

Qy 30 ELCKQF----------YHLGWVTGTGGISLKHGDE-IYIAPSGVQKERIQPEDMF 74
        || | ||| || |||| :|| ||||||||||||||
Db   4 ELFKKFSEKVEBIIEAGRILHSRGWVPATSGNISAKVSBEYIAITASGKHGKLTPEDLL 63

Qy 75 VCDINEKDISGPSPSKKLKKSQCTPLFMNAYTM-RGAGAVIHTHSKAAVMATLLFPGREF 133
        |||||||||||||||||||||| ||||| |||||||||||||||||||||||
Db 64 LIDYEGRPVGGGKPSAE------TLLHTTVYKLFPEVNAVVHTHSPNATVISIVEKKDFV 117

Qy 134 KITHQEMIKGIKKCTSGGYYRYDMLVVPIINTPEEKGLKDRMAHAMNEYPDSCAVLVR 193
        :: ||| :: :||:||||||||||||||||||||||||||
Db 118 ELEDYELLKAFP------DIHTHEVKIKIPIFPNEQNIPLLAKEVENYFKTSEDKYGFLIR 172

Qy 194 RHGVYVWGETWEKAKTMCECYDYLFDIAVSM 224
        |||:|||||||||||:: :: ::
Db 173 GHGLYTWGRSMEEALIHTEALEPIFECELKL 203

RESULT 6
D83436
probable sugar aldolase PA1683 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83436
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim.
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83436
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <STO>
A;Cross-references: UNIPROT:Q9I342; GB:AE004595; NID:g9947644; PIDN:AAG050
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1683

Query Match   12.6%;   Score 166;   DB 2;   Length 205;
Best Local Similarity   26.3%;   Pred. No. 1.6e-07;
Matches   49; Conservative 29; Mismatches 96; Indels 12; Gaps   4;

Qy 36 YHLGWVTGTGGISLKHGDE-IYIAPSGVQKERIQPEDMFVCDINEKDISGPSPSKKLKK 94
        ||| || |||| :|| ||||||||||||||||||||||||||||||||||
Db 20 YGRGWSPATSSNYSARLDEQRALLTVSGKHGQLGFDDVLA-----TDLAGNSLEPGKKP 74

Qy 95 SQCTPLFMNAYTMRGA-GAVIHTHSKAAVMATLLFPGREFKITHQEMIKGIKKCTSGGYY 153
        ||| |||||| || |||||||||||||||||||||||||||||||||
Db 75 SAETLLHTQLYAWNPAIGAVLHTHSVNATVLSRLVRGDRLVLQDYELQKAF-----AGVT 129

Qy 154 RYDMLVVPIINTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWGETWEKAKTMCEC 213
        :: || ||| :: :||:|||||
Db 130 THEGQVEVPIFDNDQDIARLASRVQPWLEAHPHCPGYLIRGHGLYTWGARMSDALRQVEA 189

Qy 214 YDYLFD 219
        :::||:
Db 190 FEFLFE 195

RESULT 7
C69054
L-fuculose-phosphate aldolase homolog - Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: C69054
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: C69054
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-191 <MTH>
A;Cross-references: UNIPROT:O27457; GB:AE000903; NID:g2622514; PIDN:AAB858
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1406
A;Start codon: GTG
C;Superfamily: L-ribulose-phosphate 4-epimerase

Query Match   11.8%;   Score 156.5;   DB 1;   Length 191;
Best Local Similarity   24.6%;   Pred. No. 1.1e-06;
Matches   52; Conservative 35; Mismatches 83; Indels 41; Gaps   8;

Qy 28 IPELCKQFYHLGWVTGTGGISLKHGDEIYIAPSGVQKERIQPEDMFVCDINEKDISGPS 87
        | : ||| ||| ||||||||| :|||||||
Db 10 VVDVSLHIYRTGLVSGIGGNVSARMGDRVFITPTMVPLGEVSLRNVVLVDLNGRVIRGGR 69

Qy 88 PSKKLKKSQCTPLFMNAYTMR-GAGAVIHTHSKAAVMATLLFPGREFKITHQEMIK---- 142
        || :|| |||||||||: | |||
Db 70 PSSEL----GLHLEVYRARPDVGGIVHTHSPHA-------RAFSIAGVQIERMEGF 114

Qy 143 -GIKKCTSGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWG 201
         | | :: : |||||||||||
Db 115 MGLGR----GY------IPMVPYHP--PGSRELAABCGRVMVDEDAAILENHGVVCAG 160

Qy 202 ETWEKAKTMCECYD------YLFDIAVSMKK 226
        ||||||||||||| ::||||||||
Db 161 EGLRDALLLAEFIEESARTQFIAETLKSMKK 191

RESULT 8
A64477
L-fuculose-phosphate aldolase homolog - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: A64477
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
Science 273, 1058-1073, 1996
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: A64477
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-181 <BUL>
A;Cross-references: UNIPROT:Q58811; GB:U67582; GB:L77117; NID:g1592064; PIDN:AAB99428.1
C;Genetics:

A;Map position: FOR1381152-1381697
C;Superfamily: L-ribulose-phosphate 4-epimerase

Query Match   11.5%;   Score 152;   DB 1;   Length 181;
Best Local Similarity   24.7%;   Pred. No. 2.5e-06;
Matches   43; Conservative   36; Mismatches   67; Indels   28; Gaps   5;

Qy   30 ELCKQFYHLGWVTGTGGISLKHGDEIYIAPSGVQKERIQPEDMFVCDINEKDISGPSPS 89
              :|| ::::|| |||:|||::| |: : ||| : :||:|| |::||
Db   8 KICRKLYDRKYVVGSGGNVSVKEGDKIYLTPTGSILGFLKEDDIAEMDLDGNVIKGKPTS 67

Qy   90 KKLKKSQCTPLFMNAYTMRG-AGAVIHTHSKAAVMATLLFPGREFKITHQEMIKGIKKCT 148
              :| : |:| ||||| |||||||||:   ::||| |||| |||:|||| ||:|
Db   68 EK------NLHLMIYRKRNDINAIIHTHSLISTFLSTI--NKEIELLTPEGKIFLKKI - 117

Qy   149 SGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWNGE 202
              :| :| :||| ||| :::: |||
Db   118 --GYVDYYEEAGSLKLAEETAKR---------------------DEDVILKNHGVVCLGK 154

RESULT 9
A72396
L-fuculose-phosphate aldolase homolog - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: A72396
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, W.C.; Ketchum, K.A.; McDonald, L.; Utterback, T.R.; Malek, J.A.; Linher, K.D.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.; Sutton, G.G.; Fleischmann, R.D.; Eisen, J.A.; White, O.; Salzberg, S.L.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: A72396
A;Status: preliminary
A;Experimental source: strain MSB8
A;Molecule type: DNA
A;Residues: 1-254 <ARN>
A;Cross-references: UNIPROT:Q9WYB9; GB:AE001710; GB:AE000512; NID:g4980775; PIDN:AAD3537
C;Genetics:
A;Gene: TMO283
C;Superfamily: L-ribulose-phosphate 4-epimerase

Query Match   11.4%;   Score 151;   DB 1;   Length 254;
Best Local Similarity   27.1%;   Pred. No. 4.7e-06;
Matches   57; Conservative   36; Mismatches   85; Indels   32; Gaps   10;

Qy   4 CDAGEGDCSRRCGAQ--DKEHPRYLIPELCKQFYHLGWVTGTGGISLKHGDEIYIAP 60
              | : :   :: :|:.| |||| ||||:||||| |||:|||:|||:|
Db   26 CCVDNFDCTFTHKGGKSMYEKERKELYNAHLLLEKY--GLVAYTSGNVSVRIGDHVLIKP 83

Qy   61 SGVQKERIQPEDMFVCDINEKDISGPSPSKKLKKSQCTPLFMNAYTMRGAGAVIHTHSKA 120
              |||:|||:|||| |::||:|||||||||||||:| |||:| ||||| |||||||||
Db   84 SGVPYTELKPEDFVVVDLEGNVIEG---EKKPSVDTATHLYLYKH-LDWAKSVIHTHSTF 139

Qy   121 AVMATLLFPGREFKITHQEMIKGIKKCTSGGYYRYDDML--VVPIIENTP-EEKGLKDRM 177
              | ||| |||| | :   :::::| :||||:||||| ||: ::: ::|:||:|
Db   140 AMWAIL-------EKSIPVL--CTA-------HADVFGEEIPLTEYAPVGSEAIGKAV 182

Qy   178 AHAMNEYPDSCAVLVRRHGVYVWGETWEKA 207
              | ||| |:||| : :::| : :|
Db   183 VKVIGK---SGAVLLRKHGVMIVGTSVDDA 209

RESULT 10
S47804
L-ribulose-phosphate 4-epimerase homolog (EC 5.1.3.-) yiaS - Escherichia coli (strain K-
N;Alternate names: hypothetical protein o231
C;Species: Escherichia coli
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S47804; A65158
R;Plunkett, G.
submitted to the EMBL Data Library, March 1994
A;Reference number: S47666

A;Accession: S47804
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-231 <PLU>
A;Cross-references: UNIPROT:P37680; EMBL:U00039; NID:g466582; PIDN:AAB18560.1; PID:g4667
A;Experimental source: strain K-12, substrain MG1655
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A65158
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-231 <BLAT>
A;Cross-references: GB:AE000435; GB:U00096; NID:g2367244; PIDN:AAC76607.1; PID:g1790008;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: yiaS
C;Superfamily: L-ribulose-phosphate 4-epimerase
C;Keywords: isomerase; zinc
F;76,95,97,171/Binding site: zinc (Asp, His, His, His) #status predicted

Query Match   11.0%;   Score 145;   DB 2;   Length 231;
Best Local Similarity   28.8%;   Pred. No. 1.5e-05;
Matches   68; Conservative   27; Mismatches   91; Indels   50; Gaps   14;

Qy   27 LIPELCKQFYHLGWVTGTGGISLKHGDE---IYIAPSGVQKERIQPEDMFVCDINEKD 82
              | |:|: | | ||||| :|:||| :| :| ::|::||::| ::
Db   10 LAANLALPAHHL--VTFTWGNVSAV--DETRQWMVIKPSGVEYDVMTADDMVVVEI----- 61

Qy   83 ISGPSPSKKLKKSQCTPLFMNAYTMRG-AGAVIHTHSKAAVM---ATLLFPGREFKITHQ 138
              |||||||||||:|||||:| ||||||| |||||||:|:| : ||||||||||||| |
Db   62 ASGKVVEGSKKPSSDTPTHLALYRRYAEIGGIVTHSRHATIWSQAGLDLPA--WGTTHA 119

Qy   139 EMIKGIKKCTS------GGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVL 191
               : :::::::| |||||||||| |||: | :|||:: |::: : ||:
Db   120 DYFYGAIPCTRQWMTAEEINGEYEYQ---TGEVIIETFEERG------RSPAQIP---AVL 167

Qy   192 VRRHGVYVWG----ETWEKAKTMCEC-YDYLFDIAVSMKKVGLDPSQLPVGENGIV 242
               :::| : | :| :| ::: : :| |:| :| ||::: :|
Db   168 VHSHGPFAWGKNAADAVHNAVVLEECAVMGLFSRQLA--------PQLPAMQNELL 215

RESULT 11
E82587
conserved hypothetical protein XF2209 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82587
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82587
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <SIM>
A;Cross-references: UNIPROT:Q9PBD5; GB:AE004033; GB:AE003849; NID:g9107342; PIDN:AAF8500
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmieri, D.A.; de Oliveira, M.C
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2209

Query Match   10.9%;   Score 144; DB 2;   Length 218;
Best Local Similarity   23.7%;   Pred. No. 1.7e-05;
Matches 49; Conservative 32; Mismatches 92; Indels 34; Gaps   8;

Qy   34 QFYHLGWVTGTGGGISLKHGD-EIYIAPSGVQKERIQPEDMFVCDINEKDISGP-SPSKK 91
            |||:|:|: ||||||:|||
Db   29 EFAQAGWTPATSSNFSHRLDEHHVAITVSGRDKRCLTEDIMAVDLEGNAVGHPHTPSAE 88

Qy   92 LKKSQCTPLFMNAY-TMRGAGAVIHTHSKAAVMATLLFPGR-EFKITHQEMIKGIKKCTS 149
            |||||| |||||||:|:||
Db   89 -----TLLHTQLYRRFPEIGCVLHTHSLTQTVASRVYAGAGHISLKDYELLKAFE---- 138

Qy   150 GGYYRYDDMLVVPIIENTPEEKGL--------KDRMAHAMNEYPDSCAVLVRRHGVVVW 200
            ||| |||
Db   139 -GHSTHETTLDVPVFCNTQNMNILAAQVDTLLDKQRM---------WGYLINGHGMYTW 187

Qy   201 GETWEKAKTMCECYDYLFDIAVSMKKV 227
            ||||| ||| :|:||
Db   188 GNTLADARRHLEALEFLLHCELNLLKL 214

RESULT 12
A95238
hypothetical protein SP2033 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: A95238
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: A95238
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-227 <KUR>
A;Cross-references: UNIPROT:Q97NJ4; GB:AE005672; PIDN:AAK76098.1; PID:g14973543; GSPDB:C
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP2033
C;Superfamily: L-ribulose-phosphate 4-epimerase

Query Match   10.7%;   Score 142; DB 2;   Length 227;
Best Local Similarity   30.8%;   Pred. No. 2.7e-05;
Matches 56; Conservative 22; Mismatches 72; Indels 32; Gaps 10;

Qy   39 GWVTGTGGGISLKHGD--EIYIAPSGVQKERIQPEDMFVCDINEKDISGPSPSKKLKKSQ 96
            ||||||:|| : ||:|: : | |||||||:|:|
Db   16 GLVKFTWGNVSEVNRELGCVIVIKPSGVDYDELTPENMVVTDLDGKILEG-----DLRPSS 70

Qy   97 CTPLFMNAY-TMRGAGAVIHTHSKAAVMATLLFPGRE---FKITHQEMIKGIKKCTSG-- 150
            ||||||||:|:|| |||||||| |||| :||:|||
Db   71 DLPTHVQLYKTWSEIGSVVHTHSTEAV-GWAQAGRDIPFYGTTHADYFYGSIPCARSLT 128

Qy   151 -----GYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVVVGWGETWE 205
            |||:|||||
Db   129 KDEVEVAYEKDTGLV--IVEBEF-EHRGLNP-----VEBVP---GIVVRNHGPFTWGKNPE 176

Qy   206 KA 207

Db   177 NA 178

RESULT 13
AI0977
probable sugar isomerase (EC 5.1.-.-) [imported] - Salmonella enterica subsp. enterica s

C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0977
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0977
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-231 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07949.1; PID:g16504938; GSPDB:GN00176
C;Genetics:
A;Gene: STY4119
C;Superfamily: L-ribulose-phosphate 4-epimerase
C;Keywords: isomerase

Query Match   10.7%;   Score 141; DB 2;   Length 231;
Best Local Similarity   30.0%;   Pred. No. 3.4e-05;
Matches 65; Conservative 26; Mismatches 84; Indels 42; Gaps 14;

Qy   39 GWVTGTGGGISLKHGDE-----IYIAPSGVQKERIQPEDMFVCDI-NEKDISGPSPSKKLK 93
            ||||||:|| |:|:
Db   20 GLVTFTWGNVSAV--DETRKLMVIKPSGVEYEVMTADDMVVVEIASGKVVEG---NKKPS 74

Qy   94 KSQCTPLFM-NAYTMRGAGAVIHTHSKAAVM---ATLLFPGREFKITHQEMIKGIKKCTS 149
            ||:|||: | || |||||||||||| :|| ||||||| |:||
Db   75 SDTATHLALYRRYPQ--IGGIVHTHSRHATIWSQAGLDLPA--WGTTHADYFYGAIPCTR 130

Qy   150 -------GGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWG- 201
            :|||:|::|| |:||:|
Db   131 LMTVEBINGEYEYQ---TGEVIIKFEERGLDPA-----QIP---AVLVHSHGPFAWGK 178

Qy   202 --ETWEKAKTMCEC-YDYLFDIAVSMKKVGLDPSQL 234
            || | || ::|:::||
Db   179 NAADAVHNAVVLEECAYMGLFSRQLAPQLPDMQPELL 215

RESULT 14
AC3533
l-fuculose phosphate aldolase (EC 4.1.2.17) [imported] - Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AC3533
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11755688
A;Accession: AC3533
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-244 <KUR>
A;Cross-references: UNIPROT:Q8YD17; GB:AE008918; PIDN:AAL53430.1; PID:g17994327; GSPDB:C
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI0189
A;Map position: II
C;Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match   10.6%;   Score 140.5; DB 2;   Length 244;
Best Local Similarity   23.8%;   Pred. No. 4e-05;
Matches 49; Conservative 31; Mismatches 67; Indels 59; Gaps   9;

Qy   25 RYLIPELCKQFYHLGWVTGTGGGISLKHGDEIYIAPSGVQKERIQPEDMFVCDINEKDIS 84
            |:||:|:
Db   37 RQSIVDAMRSFEEKGFNHGSSGNISVREGHIWVTPGA-TSTMDPQDMSLVSLEGEHLA 95

Qy   85 GPSPSKKLKKSQCTPLFMNAYTMRG--AGAVIHTHSKAAVMATLL---------F 128

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Db      96  GKIPSSEWR--------IHTEIMRAHPEAGAVVHSHADACVALSCLRKPLPFHYMIASF 147
            |  ||  |  : :    ::        ||    |||||:|: | |    |
Qy     129  PGREFKITHQEMIKGIKKCTSGGYYRY--DDMLVVPIIENTPEEKGLKDRMAHAMNEYPD 186
            |||                    |:        ::
Db     148  GGSEV----------PCAS---YRVFGSDALAYEVV-------------RAMGHHR- 177

Qy     187  SCAVLVRRHGVYVWGETWEKAKTMCE 212
            :| : || :||| |||  |: : |
Db     178  --ACLMASHGMVVWGRDLAHARLLAE 201


RESULT 15
B98102
L-ribulose-phosphate 4-epimerase (EC 5.1.3.4) [imported] - Streptococcus pneumoniae (str
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: B98102
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: B98102
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-234 <KUR>
A;Cross-references: UNIPROT:Q8DN99; GB:AE007317; PIDN:AAL00647.1; PID:g15459534; GSPDB:G
C;Genetics:
A;Gene: araD
C;Superfamily: L-ribulose-phosphate 4-epimerase
C;Keywords: isomerase

Query Match             10.4%;  Score 137;  DB 2;  Length 234;
Best Local Similarity   30.2%;  Pred. No. 7.8e-05;
Matches    55;  Conservative   22;  Mismatches   73;  Indels   32;  Gaps   10;

Qy      39  GWVTGTGGGISLKHGD--BIYIAPSGVQKERIQPEDMFVCDINEKDISGPSPSKKLKKSQ 96
            |          | ||    |||||  :: :|||   ||:| ||:
Db      23  GLVKFTWGNVSEVNRELGVIVIKPSGVDYDELITPENMVVTDLDGKILEG-----DLRPSS 77

Qy      97  CTPLFMNAY-TMRGAGAVIHTHSKAAVMATLLFPGRE---FKITHQEMIKGIKKCTSG-- 150
            |:|:||||  |: |||||:||||                  ||:||||| :||||
Db      78  DLPTHVQLYKAWSEIGSVVHTHSTEAV--GWAQAGRDIPFYGTTHADYFYGSIPCARSLT 135

Qy     151  -----GYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWGETWE 205
                 |:| ||:|| |: |||  ||    ::||||||||:   :: ||||||| |||
Db     136  KDEVEVAYEKDTGLV--IVEEF-EHRGLNP------VEVP---GIVVRNHGPFTWGKNPE 183

Qy     206  KA 207
            |
Db     184  NA 185


Search completed: February 1, 2005, 14:30:13
Job time : 42 secs
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